

Additional file 1

Title: Target abundance of RNA transcripts

Evaluation of target abundance; i.e., whether low abundant RNA transcripts (RNA transcripts with Cq-values above 30 cycles) could be detected in blood-RNA samples isolated using the five blood-RNA isolation protocols. Low abundant mRNA and miRNA transcripts were detected in all analyzed samples. The average of non-normalized raw Cq-values of all targets from all adult (n=11-12 Tempus tubes) and cord blood (n=3-6 Tempus tubes) samples collected in the Tempus tubes of the blood-RNA samples isolated using the five RNA isolation protocols.

Table 1. Target abundance of RNA transcripts

Gene name	Average Cq \pm SD
High abundant target (Cq < 25)	
hsa-let-7a	18.31 \pm 1.95
hsa-miR-16	16.87 \pm 2.65
hsa-miR-20a	23.44 \pm 2.99
hsa-miR-21	24.86 \pm 2.20
hsa-miR-191	21.61 \pm 2.50
hsa-miR-451	23.17 \pm 4.04
Medium abundant target (25 \leq Cq \leq 30)	
FOS	28.39 \pm 0.85
IL1B	29.65 \pm 0.68
TP53	29.46 \pm 0.54
hsa-miR-26a	29.26 \pm 3.44
hsa-miR-93	28.27 \pm 3.21
hsa-miR-192	25.54 \pm 1.93
Low abundant target (Cq > 30)	
CDKN1A	32.48 \pm 0.64
IL8	32.19 \pm 1.26
MYC	30.08 \pm 0.83
hsa-miR-34a	31.24 \pm 2.10
hsa-miR-103	31.46 \pm 3.21
hsa-miR-126	30.27 \pm 2.63
hsa-miR-423-3p	30.30 \pm 3.08